

**IN THE ABSTRACT:**

Please amend the abstract as follows:

The method and system for identifying a biological sample generates a data set indicative of the composition of the biological sample. In a particular example, the data set is DNA spectrometry data received from a mass spectrometer. The data set is denoised, and a baseline is deleted. Since possible compositions of the biological sample may be known, expected peak areas may be determined. Using the expected peak areas, a residual baseline is generated to further correct the data set. Probable peaks are then identifiable in the corrected data set, which are used to identify the composition of the biological sample. In a disclosed example, statistical methods are employed to determine the probability that a probable peak is an actual peak, not an actual peak, or that the data are too inconclusive to call.

**IN THE CLAIMS:**

Please amend claims 2-37, 39, and 40 as follows:

2. (Amended) The method according to claim 1, wherein the data set is a spectrometry data set.
3. (Amended) The method according to claim 1, wherein the data set is generated by a mass spectrometer.
4. (Amended) The method according to claim 1, wherein denoising the data set includes generating a noise profile for the data set.
5. (Amended) The method according to claim 1, wherein denoising the data set includes transforming the data set using wavelet technology into a series of stages.
6. (Amended) The method according to claim 5, further including generating a noise profile for stage 0.
7. (Amended) The method according to claim 6, further including generating a noise profile for other stages.